SEQUENCE LISTING

<110> THOMAS JEFFERSON UNIVERSITY
UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION

<120> METHODS AND COMPOSITIONS FOR INHIBITING CHOLESTEROL UPTAKE

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<141> 2004-02-03

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<151> 2003-02-03

<160> 13

<170> PatentIn Ver. 3.2

<210> 1
<211> 339
<212> PRT
<213> Homo sapiens

<400> 1

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Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp
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His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr Asn
            20                  25                  30

Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys Thr
        35                  40                  45

Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg Ser
    50                  55                  60

Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr Lys
65                  70                  75                  80

Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu Glu
                85                  90                  95

Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala Ser
            100                 105                 110

Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser Leu
        115                 120                 125

Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile Asn
    130                 135                 140

Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile Ile
145                 150                 155                 160

Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala Lys
                165                 170                 175

Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile Asp
            180                 185                 190
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Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly Thr
        195                 200                 205

Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Val Pro His
    210                 215                 220

Leu Gln Lys Val Phe Asp Arg Tyr Lys Ser Tyr Ser Pro Tyr Asp Met
225                 230                 235                 240

Leu Glu Ser Ile Arg Lys Glu Val Lys Gly Asp Leu Glu Asn Ala Phe
                245                 250                 255

Leu Asn Leu Val Gln Cys Ile Gln Asn Lys Pro Leu Tyr Phe Ala Asp
            260                 265                 270

Arg Leu Tyr Asp Ser Met Lys Gly Lys Gly Thr Arg Asp Lys Val Leu
        275                 280                 285

Ile Arg Ile Met Val Ser Arg Ser Glu Val Asp Met Leu Lys Ile Arg
    290                 295                 300

Ser Glu Phe Lys Arg Lys Val Gly Lys Ser Leu Tyr Tyr Tyr Ile Gln
305                 310                 315                 320

Gln Asp Thr Lys Gly Asp Tyr Gln Lys Ala Leu Leu Tyr Leu Cys Gly
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Gly Asp Asp
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<210> 2
<211> 337
<212> PRT
<213> Danio rerio

<400> 2

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Met Ala Leu Val Ser Glu Tyr Leu Ser Lys Leu Thr Leu Ser Tyr Gly
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Gly Glu Arg Glu Pro Lys Cys Pro Thr Val Val Ala Ala Tyr Asp Phe
            20                  25                  30

Asn Pro Glu Val Asp Ala Ala Lys Ile Glu Thr Ala Ile Lys Thr Lys
        35                  40                  45

Gly Val Asp Glu Gln Thr Ile Ile Asp Ile Leu Thr Arg Arg Ser Leu
    50                  55                  60

Leu Lys Arg Ser Asp Ile Ala Phe Glu Tyr Glu Lys Arg Ala Lys Lys
65                  70                  75                  80

Asp Leu Val Ser Ala Leu Lys Gly Ala Leu Ser Gly Ser Leu Glu His
                85                  90                  95

Leu Ile Leu Gly Leu Met Lys Ser Thr Pro Gln Tyr Asp Ala Phe Glu
            100                 105                 110

Leu Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Leu Ile Glu
        115                 120                 125
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Met Val Cys Ser Arg Asn Lys Glu Glu Leu Ala Glu Ile Lys Lys Val
    130                 135                 140

Tyr Lys Glu Met Phe Lys Lys Asp Leu Glu Lys Asp Ile Ser Gly Asp
145                 150                 155                 160

Thr Ser Gly Asp Phe Ala Lys Leu Leu Leu Ala Leu Ala Gln Gly Asn
                165                 170                 175

Arg Glu Glu Gln Ser Ser Val Val Asp Tyr Glu Lys Ile Asp Asn Asp
            180                 185                 190

Ala Arg Thr Leu Tyr Glu Thr Gly Val Arg Arg Lys Gly Thr Asp Val
        195                 200                 205

Val Thr Trp Ile Ser Ile Phe Ser Glu Arg Ser Val Ser His Leu Gln
    210                 215                 220

Lys Val Phe Glu Arg Tyr Lys Arg Tyr Ser Pro Tyr Asp Leu Lys Glu
225                 230                 235                 240

Ser Ile Arg Met Glu Val Lys Gly Asp Leu Glu Lys Ser Phe Leu Thr
                245                 250                 255

Leu Val Glu Cys Leu Glu Asn Lys His Leu Tyr Phe Ala Ser Arg Leu
            260                 265                 270

Asn Asp Ala Met Lys Gly Lys Ser Val Lys Asp Lys Ile Ile Thr Arg
        275                 280                 285

Ile Ile Val Ser Arg Cys Glu Val Asp Leu Met Lys Val Arg Ile Glu
    290                 295                 300

Phe Lys Arg Asn Phe Gly Arg Ser Leu His Gln Thr Ile Ser Glu His
305                 310                 315                 320

Thr Lys Gly Asp Tyr Gln Arg Ala Leu Leu Asn Leu Val Gly Gly Asp
                325                 330                 335

Asp
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<210> 3
<211> 181
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<213> Danio rerio

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Ser Pro Phe Ile Arg Lys Gln Gly Asn Ile Tyr Lys Pro Asn Asn Lys
            20                  25                  30

Glu Met Asp Asn Asp Ser Ile Asn Glu Lys Thr Leu Gln Asp Val His
        35                  40                  45

Thr Lys Glu Ile Asp Leu Val Asn Arg Asp Pro Lys His Leu Asn Asp
    50                  55                  60

Asp Val Val Lys Val Asp Phe Glu Asp Val Ile Ala Glu Pro Ala Gly
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65 70 75 80

Thr Tyr Ser Phe Asp Gly Val Trp Lys Ala Ser Phe Thr Thr Phe Thr
85 90 95

Val Thr Lys Tyr Trp Cys Tyr Arg Leu Leu Thr Ala Leu Val Gly Ile
100 105 110

Pro Leu Ala Leu Val Trp Gly Ile Phe Phe Ala Ile Leu Ser Phe Ile
115 120 125

His Ile Trp Ala Val Val Pro Cys Val Lys Ser Tyr Leu Ile Glu Ile
130 135 140

His Cys Ile Ser Arg Val Tyr Ser Ile Cys Val His Thr Phe Cys Asp
145 150 155 160

Pro Leu Phe Glu Ala Met Gly Lys Cys Phe Ser Asn Val Arg Val Thr
165 170 175

Ala Thr Lys Val Val
180

<210> 4
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<212> PRT
<213> Homo sapiens

<400> 4
Met Ser Gly Gly Lys Tyr Val Asp Ser Glu Gly His Leu Tyr Thr Val
1 5 10 15

Pro Ile Arg Glu Gln Gly Asn Ile Tyr Lys Pro Asn Asn Lys Ala Met
20 25 30

Ala Asp Glu Leu Ser Glu Lys Gln Val Tyr Asp Ala His Thr Lys Glu
35 40 45

Ile Asp Leu Val Asn Arg Asp Pro Lys His Leu Asn Asp Asp Val Val
50 55 60

Lys Ile Asp Phe Glu Asp Val Ile Ala Glu Pro Glu Gly Thr His Ser
65 70 75 80

Phe Asp Gly Ile Trp Lys Ala Ser Phe Thr Thr Phe Thr Val Thr Lys
85 90 95

Tyr Trp Phe Tyr Arg Leu Leu Ser Ala Leu Phe Gly Ile Pro Met Ala
100 105 110

Leu Ile Trp Gly Ile Tyr Phe Ala Ile Leu Ser Phe Leu His Ile Trp
115 120 125

Ala Val Val Pro Cys Ile Lys Ser Phe Leu Ile Glu Ile Gln Cys Ile
130 135 140

Ser Arg Val Tyr Ser Ile Tyr Val His Thr Val Cys Asp Pro Leu Phe
145 150 155 160

Glu Ala Val Gly Lys Ile Phe Ser Asn Val Arg Ile Asn Leu Gln Lys

165 170 175

Glu Ile

<210> 5
<211> 19
<212> PRT
<213> Danio rerio

<220>
<221> MOD_RES
<222> (7)
<223> unidentified amino acid

<220>
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<223> unidentified amino acid

<220>
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<222> (17)
<223> unidentified amino acid

<400> 5
Met Thr Ser Gly Tyr Lys Xaa Gly Thr Pro Glu Glu Xaa Tyr Ala His
1 5 10 15

Xaa Pro Glu

<210> 6
<211> 16
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<213> Danio rerio

<220>
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<220>
<221> MOD_RES
<222> (14)
<223> unidentified amino acid

<400> 6
Glu Xaa Asp Asn Asp Ser Ile Asn Glu Xaa Thr Leu Gln Xaa Val His
1 5 10 15

<210> 7
<211> 12
<212> PRT
<213> Danio rerio

<220>
<221> MOD_RES
<222> (9)
<223> unidentified amino acid

<400> 7
Leu Thr Leu Ser Tyr Gly Gly Glu Xaa Glu Pro Lys
1 5 10

<210> 8
<211> 14
<212> PRT
<213> Danio rerio

<400> 8
Arg Ser Leu Leu Lys Arg Ser Asp Ile Ala Phe Glu Tyr Glu
1 5 10

<210> 9
<211> 13
<212> PRT
<213> Danio rerio

<220>
<221> MOD_RES
<222> (4)
<223> unidentified amino acid

<220>
<221> MOD_RES
<222> (11)
<223> unidentified amino acid

<400> 9
Val Phe Glu Xaa Tyr Lys Arg Tyr Ser Pro Xaa Asp Leu
1 5 10

<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 10
tgtcccgtcc ttgtatccgc tagtc 25

<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

oligonucleotide

<400> 11
gccattttcc ttagttgttg tagag 25

<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 12
gccaatttcg ttagtagttg aagag 25

<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 13
ctaagaactc agagaccaaa gccat 25